WHAT IS CLAIMED IS:

1. A method for identifying a polynucleotide in a liquid phase comprising:

a) contacting a plurality of polynucleotides derived from at least one organism with at least one nucleic acid probe under conditions that allow hybridization of the probe to the polynucleotides having complementary sequences, wherein the probe is labeled with a detectable molecule; and

b) identifying a polynucleotide of interest with an analyzer that detects the detectable molecule.

2. The method of claim 1, wherein the polynucleotides are from a mixed population of cells.

3. The method of claim 1, wherein the polynucleotides are in a library.

4. The method of claim 3 wherein the library is an expression library.

5. The method of claim 3 wherein the library is an environmental expression library.

6. The method of claim 1, wherein the nucleic acid probe is from at least about 15 bases to about 100 bases.

7. The method of claim 1, wherein the nucleic acid probe is from at least about 100 bases to about 500 bases.

8. The method of claim 1, wherein the nucleic acid probe is from at least about 500 bases to about 1,000 bases.

9. The method of claim 1, wherein the nucleic acid probe is from at least about 1,000 bases to about 5,000 bases.

10. The method of claim 1, wherein the nucleic acid probe is from at least about 5,000 bases to about 10,000 bases.

11. The method of claim 1, wherein the detectable molecule is a fluorescent molecule.

12. The method of claim 1, wherein the detectable molecule is a magnetic molecule.

13. The method of claim 1, wherein the detectable molecule modulates a magnetic field.

14. The method of claim 1, wherein the detectable molecule modulates the dielectric signature of the clone.

15. The method of claim 1, wherein the analyzer is a FACS analyzer.

16. The method of claim 1, wherein the analyzer is a magnetic field sensing device.

17. The method of claim 9, wherein the magnetic field sensing device is a Super Conducting Quantum Interference Device.

18. The method of claim 1, wherein the analyzer is a multipole coupling spectroscopy device.

19. The method of claim 1, wherein the organism is from an environmental sample.

20. The method of claim -1, wherein the environmental sample is selected from the group consisting of: geothermal fields, hydrothermal fields, acidic soils, sulfotara mud pots, boiling mud pots, pools, hot-springs, geysers, marine actinomycetes, metazoan, endosymbionts, ectosymbionts, tropical soil, temperate soil, arid soil, compost piles, manure piles, marine sediments, freshwater sediments, water concentrates, hypersaline sea ice, super-cooled sea ice, arctic tundra, Sargosso sea, open ocean pelagic, marine snow, microbial mats, whale falls, springs, hydrothermal vents, insect and nematode gut microbial communities, plant endophytes, epiphytic water samples, industrial sites and ex situ enrichments.

21. The method of claim -2, wherein the environmental sample is selected from the group consisting of: eukaryotes, prokaryotes, myxobacteria (epothilone), air, water, sediment, soil or rock.

22. The method of claim 1, wherein the organism comprises a microorganism.

23. The method of claim 19, wherein the environmental sample contains extremophiles.

24. The method of claim 23, wherein the extremophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acidophiles.

25. The method of claim 1, further comprising encapsulation of the polynucleotide in a microenvironment.

26. The method of claim 25, wherein the microenvironment is selected from beads, high temperature agaroses, gel microdroplets, cells, ghost red blood cells, macrophages, or liposomes.

27. The method of claim 26, wherein the microenvironment is a gel microdroplet.

28. The method of claim 25, wherein the detectable molecule is a biotinylated substrate.

29. The method of claim 28, wherein the biotinylated substrate comprises a core fluorophore structure, a spacer connected to the fluorophore structure by a first connector and connected to the bioactivity or biomolecume of interest by a second connector, and two functional groups, wherein each functional group is attached to the fluorophore structure by a connector unit.

30. The method of claim 29, wherein the fluorophore is selected from the group consisting of coumarins, resorufins and xanthenes.

31. The method of claim 29, wherein the spacer is selected from the group consisting of: alkanes, and oligoethyleneglycols.

32. The method of claim 29, wherein the connector units are selected from the groups consisting of ether, amine, amide, ester, urea, thiourea and other moieties.

33. The method of claim 29, wherein the functional groups are independently selected from the group consisting of straight alkanes, branched alkanes, monosaccharides, oligosaccharides, unsaturated hydrocarbons and aromatic groups.

34. The method of claim 25, wherein the analyzer is a flow cytometer.

35. The method of claim 28, wherein the biotinylated substrate comprises a core fluorophore structure, a spacer connected to the fluorophore structure by a first connector and connected to the bioactivity or biomolecule of interest by a second connector, and a quencher component, attached to the cluorophore by a polymer.

36. The method of claim 35, wherein the fluorophore is selected from the group consisting of acridines, coumarins, fluorescein, rhodamine, BOPIDY, resorufin, and porphyrins.

37. The method of claim 35, wherein the quencher is a moiety capable of quenching fluorescence of the fluorophore.

38. The method of claim 35, wherein the polymer is selected from the group consisting of amines, ethers, esters, amides, peptides and oligosaccharides.

39. The method of claim 35, wherein the spacer is selected from the group consisting of: alkanes, and oligoethyleneglycols.

40. The method of claim 35, wherein the first and second connectors are selected from the groups consisting of ether, amine, amide, ester, urea, thiourea and other moieties.

41. The method of claim 1, wherein the polynucleotide of interest encodes an enzyme.

42. The method of claim 41, wherein the enzyme is selected from the group consisting of lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases,

mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, eposize hydrolases, nitrile hydratases, nitrilases, transaminases, amidases, and acylases.

43. The method of claim 1, wherein the polynucleotide of interest encodes a small molecule.

44. The method of claim 1, wherein the polynucleotide of interest, or fragments thereof, comprise one or more operons, or portions thereof.

45. The method of claim 44, wherein the operons, or portions thereof, encodes a complete or partial metabolic pathway.

46. The method of claim 44, wherein the operons or portions thereof encoding a complete or partial metabolic pathway encodes polyketide syntheses.

47. A method for identifying a polynucleotide encoding a polypeptide of interest comprising:

co-encapsulating in a microenvironment a plurality of library clones containing DNA obtained from a mixed population of organisms, with a mixture of oligonucleotide probes comprising a detectable label and at least a portion of a polynucleotide sequence encoding a polypeptide of interest having a specified bioactivity under such conditions and for such time as to allow interaction of complementary sequences; and

identifying clones containing a complement to the oligonucleotide probe encoding the polypeptide of interest by separating clones with an analyzer that detects the detectable label.

48. A method for high throughput screening of a polynucleotide library for a polynucleotide of interest that encodes a molecule of interest, comprising:

(a) contacting a library containing a plurality of clones comprising polynucleotides derived from a mixed population of organisms with a plurality of oligonucleotide probes labeled with a detectable molecule; and

(b) separating clones with an analyzer that detect the detectable molecule.

49. The method of claim 48, further comprising:

(a) contacting the separated clones with a reporter system that identifies a polynucleotide encoding the molecule of interest; and

(b) identifying clones capable of modulating expression or activity of the reporter system thereby identifying a polynucleotide of interest.

50. The method of claim 48, wherein the library is an expression library.

51. The method of claim 48, wherein the mixed population of organisms is from an environmental sample.

52. The method of claim 51, wherein the environmental sample is selected from the group consisting of: geothermal fields, hydrothermal fields, acidic soils, sulfotara mud pots, boiling mud pots, pools, hot-springs, geysers, marine actinomycetes, metazoan, endosymbionts, ectosymbionts, tropical soil, temperate soil, arid soil, compost piles, manure piles, marine sediments, freshwater sediments, water concentrates, hypersaline sea ice, super-cooled sea ice, arctic tundra, Sargosso sea, open ocean pelagic, marine snow, microbial mats, whale falls, springs, hydrothermal vents, insect and nematode gut microbial communities, plant endophytes, epiphytic water samples, industrial sites and ex situ enrichments.

53. The method of claim 51, wherein the environmental sample is selected from the group consisting of: eukaryotes, prokaryotes, myxobacteria (epothilone), air, water, sediment, soil or rock.

54. The method of claim 48, wherein the mixed population of organisms comprises microorganisms.

55. The method of claim 51, wherein the environmental sample contains extremophiles.

56. The method of claim 55, wherein the extremophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acidophiles.

57. The method of claim 49, wherein the reporter system is a bioactive substrate.

58. The method of claim 57, wherein the bioactive substrate comprises C12FDG.

59. The method of claim 58, wherein the bioactive substrate further comprises a lipophilic tail.

60. The method of claim 49, further comprising prior to (a):
    (i) obtaining polynucleotides from a mixed population of organisms; and
    (ii) generating a polynucleotide library.

61. The method of claim 60, further comprising normalizing the polynucleotides prior to generating the library.

62. The method of claim 48, further comprising encapsulation of the clones in a gel microdrop.

63. The method of claim 62, wherein the detectable molecule is a biotinylated substrate.

64. The method of claim 63, wherein the biotinylated substrate comprises a core fluorophore structure, a spacer connected to the fluorophore structure by a first connector and connected to the bioactivity or biomolecume of interest by a second connector, and two functional groups, wherein each functional group is attached to the fluorophore structure by a connector unit.

65. The method of claim 64, wherein the fluorophore is selected from the group consisting of coumarins, resorufins and xanthenes.

66. The method of claim 64, wherein the spacer is selected from the group consisting of: alkanes, and oligoethyleneglycols.

67. The method of claim 64, wherein the connector units are selected from the groups consisting of ether, amine, amide, ester, urea, thiourea and other moieties.

68. The method of claim 64, wherein the functional groups are independently selected from the group consisting of straight alkanes, branched alkanes, monosaccharides, oligosaccharides, unsaturated hydrocarbons and aromatic groups.

69. The method of claim 62, wherein the analyzer is a flow cytometer.

70. The method of claim 63, wherein the biotinylated substrate comprises a core fluorophore structure, a spacer connected to the fluorophore structure by a first connector and connected to the bioactivity or biomolecule of interest by a second connector, and a quencher component, attached to the cluorophore by a polymer.

71. The method of claim 70, wherein the fluorophore is selected from the group consisting of acridines, coumarins, fluorescein, rhodamine, BOPIDY, resorufin, and porphyrins.

72. The method of claim 70, wherein the quencher is a moiety capable of quenching fluorescence of the fluorophore.

73. The method of claim 70, wherein the polymer is selected from the group consisting of amines, ethers, esters, amides, peptides and oligosaccharides.

74. The method of claim 70, wherein the spacer is selected from the group consisting of: alkanes, and oligoethyleneglycols.

75. The method of claim 70, wherein the first and second connectors are selected from the groups consisting of ether, amine, amide, ester, urea, thiourea and other moieties.

76. The method of claim 48, wherein the polynucleotide of interest encodes an enzyme.

77. The method of claim 76, wherein the enzyme is selected from the group consisting of lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases, mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, eposize hydrolases, nitrile hydratases, nitrilases, transaminases, amidases, and acylases.

78. The method of claim 49, wherein the reporter system comprises a detectable label.

79. The method of claim 49, wherein the reporter system comprises a first test protein linked to a DNA binding moiety and a second test protein linked to a transcriptional activation moiety, wherein modulation of the interaction of the first test protein linked to a DNA binding moiety with the second test protein linked to a transcription activation moiety results in a change in the expression of a detectable protein.

80. The method of claim 49, wherein the polynucleotide of interest encodes a small molecule.

81. The method of claim 49, wherein the polynucleotide of interest, or fragments thereof, comprise one or more operons, or portions thereof.

82. The method of claim 81, wherein the operons, or portions thereof, encodes a complete or partial metabolic pathway.

83. The method of claim 82, wherein the operons or portions thereof encoding a complete or partial metabolic pathway encodes polyketide syntheses.

84. The method of claim 48, wherein the analyzer is a fluorescence activated cell sorting (FACS) apparatus.

85. The method of claim 48, wherein the analyzer is a magnetic field sensing device.

86. The method of claim 85, wherein the magnetic field sensing device is a Super Conducting Quantum Interference Device.

87. The method of claim 48, wherein the analyzer is a multipole coupling spectroscopy device.

88. The method of claim 48, wherein the plurality of oligonucleotide probes have different nucleic acid sequences.

89. The method of claim 88, wherein the sequences are portions of a polynucleotide encoding a molecule of interest.

90. The method of claim 48, wherein the plurality of oligonucleotide probes have the same nucleic acid sequence.

91. A method of screening for a polynucleotide encoding an activity of interest, comprising:

(a) obtaining polynucleotides from an environmental sample;

(b) normalizing the polynucleotides obtained from the sample;

(c) generating a library from the normalized polynucleotides;

(d) contacting the library with a plurality of oligonucleotide probes comprising a detectable label and at least a portion of a polynucleotide sequence encoding a polypeptide of interest having a specified activity to select library clones positive for a sequence of interest; and

(e) selecting clones with an analyzer that detects the detectable label.

92. The method of claim 91, further comprising:

(a) contacting the selected clones with a reporter system that identifies a polynucleotide encoding the activity of interest; and

(b) identifying clones capable of modulating expression or activity of the reporter system thereby identifying a polynucleotide of interest; wherein the positive clones contain a polynucleotide sequence encoding an activity of interest which is capable of catalyzing the bioactive substrate.

93. A method for screening polynucleotides, comprising:

(a) contacting a library of polynucleotides wherein the polynucleotides are derived from a mixed population of organism with a probe oligonucleotide labeled with a fluorescence molecule, which fluoresce upon binding of the probe to a target polynucleotide of the library, to select library polynucleotides positive for a sequence of interest;

(b) separating library members that are positive for the sequence of interest with a fluorescent analyzer that detects fluorescence; and

(c) expressing the selected polynucleotides to obtain polypeptides.

94. The method of claim 93, further comprising:

(a) contacting the polypeptides with a reporter system; and

(b) identifying polynucleotides encoding polypeptides capable of modulating expression or activity of the reporter system.

95. A method for obtaining an organism from a mixed population of organisms in a sample comprising:

(a) encapsulating in a microenvironment at least one organism from the sample;

(b) incubating the encapsulated at least one organism under such conditions and for such a time to allow the at least one microorganism to grow or proliferate; and

(c) sorting the encapsulated at least one organism by a flow cytometer to obtain an organism from the sample.

96. The method of claim 95, wherein the mixed population of organisms is from an environmental sample.

97. The method of claim 96, wherein the environmental sample is selected from the group consisting of: geothermal fields, hydrothermal fields, acidic soils, sulfotara mud pots, boiling mud pots, pools, hot-springs, geysers, marine actinomycetes, metazoan, endosymbionts, ectosymbionts, tropical soil, temperate soil, arid soil, compost piles, manure piles, marine sediments, freshwater sediments, water concentrates, hypersaline sea ice, super-cooled sea ice, arctic tundra, Sargosso sea, open ocean pelagic, marine snow, microbial mats, whale falls, springs, hydrothermal vents, insect and nematode gut microbial communities, plant endophytes, epiphytic water samples, industrial sites and ex situ enrichments.

98. The method of claim 96, wherein the environmental sample is selected from the group consisting of: eukaryotes, prokaryotes, myxobacteria (epothilone), air, water, sediment, soil or rock.

99. The method of claim 95, wherein the mixed population of organisms comprises microorganisms.

100. The method of claim 96, wherein the environmental sample contains extremophiles.

101. The method of claim 101, wherein the extremophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acidophiles.

102. The method of claim 95, wherein the flow cytometer comprises a magnetic field sensing device.

103. The method of claim 102, wherein the magnetic field sensing device is a Super Conducting Quantum Interference Device.

104. The method of claim 95, wherein the flow cytometer is a multipole coupling spectroscopy device.

105. A method for identifying a bioactivity or biomolecule of interest, comprising:

(a) transferring a library containing a plurality of clones comprising polynucleotides derived from a mixed population of organisms or more than one organism, to a bacterial host cell;

(b) contacting the bacterial host cell with a mammalian host cell containing a detectable reporter molecule in a microenvironment; and

(c) separating clones with an analyzer that detects the detectable molecule.

106. The method of claim 105, wherein the microenvironment is selected from beads, high temperature agaroses, gel microdroplets, cells, ghost red blood cells, macrophages, or liposomes.

107. The method of claim 106, wherein the liposomes are prepared from one or more phospholipids, glycolipids, steroids, alkyl phosphates or fatty acid esters.

108. The method of claim 107, wherein the phospholipids are selected from the group consisting of lecithin, sphingomyelin and dipalmitoyl.

109. The method of claim 107, wherein the steroids are selected from the group consisting of cholesterol, cholestanol and lanosterol.

110. The method of claim 105, wherein the detectable reporter contains a bioluminescent molecule, a chemiluminescent molecule, a colorimetric molecule, an electromagnetic molecule, an isotopic molecule, a thermal molecule or an enzymatic substrate.

111. The method of claim 110, wherein the bioluminescent molecule is green fluorescent protein (GFP) or red fluorescent protein (RFP).

112. The method of claim 105, wherein the analyzer is a FACS analyzer.

113. The method of claim 105, wherein the analyzer is capillary-based screening apparatus.

114. A method for identifying a bioactivity or biomolecule of interest, comprising:

(a) transferring a library containing a plurality of clones comprising polynucleotides derived from a mixed population of organisms or more than one organism, to a first host cell;

(b) contacting the first host cell with a second host cell containing a detectable reporter molecule in a microenvironment, wherein the first host cell is different from the second host cell; and

(c) separating clones with an analyzer that detects the detectable molecule.

115. The method of claim 114, wherein the first host cell is a prokaryotic cell.

116. The method of claim 114, wherein the first host cell is a eukaryotic cell.

117. The method of claim 114, wherein the second host cell is a prokaryotic cell.

118. The method of claim 114, wherein the second host cell is a eukaryotic cell.

119. The method of claims 115 or 117, wherein the prokaryotic cell is a bacterial cell.

120. The method of claims 116 or 118, wherein the eukaryotic cell is a mammalian cell.

121. The method of claim 114, wherein the microenvironment is selected from beads, high temperature agaroses, gel microdroplets, cells, ghost red blood cells, macrophages, or liposomes.

122. The method of claim 121, wherein the liposomes are prepared from one or more phospholipids, glycolipids, steroids, alkyl phosphates or fatty acid esters.

123. The method of claim 122, wherein the phospholipids are selected from the group consisting of lecithin, sphingomyelin and dipalmitoyl.

124. The method of claim 122, wherein the steroids are selected from the group consisting of cholesterol, cholestanol and lanosterol.

125. The method of claim 114, wherein the detectable reporter contains a bioluminescent molecule, a chemiluminescent molecule, a colorimetric molecule, an electromagnetic molecule, an isotopic molecule, a thermal molecule or an enzymatic substrate.

126. The method of claim 125, wherein the bioluminescent molecule is green fluorescent protein (GFP) or red fluorescent protein (RFP).

127. The method of claim 114, wherein the analyzer is a FACS analyzer.

128. The method of claim 114, wherein the analyzer is capillary-based screening apparatus.

129. A method for identifying a bioactivity or biomolecule of interest, comprising:

(a) transferring a library containing a plurality of clones comprising polynucleotides derived from a mixed population of organisms or more than one organism, to a host cell; and

(b) contacting the first host cell with a second host cell containing a detectable reporter molecule in a microenvironment, wherein the first host cell and second host cell are different.

130. The method of claim 129, wherein the first host cell is a prokaryotic cell.

131. The method of claim 129, wherein the first host cell is a eukaryotic cell.

132. The method of claim 129, wherein the second host cell is a prokaryotic cell.

133. The method of claim 129, wherein the second host cell is a eukaryotic cell.

134. The method of claims 130 or 132, wherein the prokaryotic cell is a bacterial cell.

135. The method of claims 131 or 133, wherein the eukaryotic cell is a mammalian cell.

136. The method of claim 129, wherein the microenvironment is selected from beads, high temperature agaroses, gel microdroplets, cells, ghost red blood cells, macrophages, or liposomes.

137. The method of claim 136, wherein the liposomes are prepared from one or more phospholipids, glycolipids, steroids, alkyl phosphates or fatty acid esters.

138. The method of claim 137, wherein the phospholipids are selected from the group consisting of lecithin, sphingomyelin and dipalmitoyl.

139. The method of claim 137, wherein the steroids are selected from the group consisting of cholesterol, cholestanol and lanosterol.

140. The method of claim 129, wherein the detectable reporter contains a bioluminescent molecule, a chemiluminescent molecule, a colorimetric molecule, an electromagnetic molecule, an isotopic molecule, a thermal molecule or an enzymatic substrate.

141. The method of claim 140, wherein the bioluminescent molecule is green fluorescent protein (GFP) or red fluorescent protein (RFP).

142. The method of claim 129, further comprising separating the clones with an analyzer that detects the detectable molecule.

143. The method of claim 142, wherein the analyzer is a FACS analyzer.

144. The method of claim 142, wherein the analyzer is a capillary-based screening apparatus.

145. The method of claim 142, wherein the analyzer is a mass spectroscopic screening apparatus.

146. A method for identifying a bioactivity or biomolecule of interest, comprising:

(a) transferring the extract of a library containing a plurality of clones comprising polynucleotides derived from a mixed population of organisms or more than one organism, to a first host cell; and

(b) contacting the extract with a second host cell containing a detectable reporter molecule.

147. The method of claim 146, wherein the first host cell is a prokaryotic cell.

148. The method of claim 146, wherein the first host cell is a eukaryotic cell.

149. The method of claim 146, wherein the second host cell is a prokaryotic cell.

150. The method of claim 146, wherein the second host cell is a eukaryotic cell.

151. The method of claims 147 or 149, wherein the prokaryotic cell is a bacterial cell.

152. The method of claims 148 or 150, wherein the eukaryotic cell is a mammalian cell.

153. The method of claim 146, wherein the extract is contacted with a host cell in a microenvironment.

154. The method of claim 153, wherein the microenvironment is selected from beads, high temperature agaroses, gel microdroplets, cells, ghost red blood cells, macrophages, or liposomes.

155. The method of claim 154, wherein the liposomes are prepared from one or more phospholipids, glycolipids, steroids, alkyl phosphates or fatty acid esters.

156. The method of claim 155, wherein the phospholipids are selected from the group consisting of lecithin, sphingomyelin and dipalmitoyl.

157. The method of claim 155, wherein the steroids are selected from the group consisting of cholesterol, cholestanol and lanosterol.

158. The method of claim 146, wherein the detectable reporter contains a bioluminescent molecule, a chemiluminescent molecule, a colorimetric molecule, an electromagnetic molecule, an isotopic molecule, a thermal molecule or an enzymatic substrate.

159. The method of claim 158, wherein the bioluminescent molecule is green fluorescent protein (GFP) or red fluorescent protein (RFP).

160. The method of claim 146, further comprising separating the clones with an analyzer that detects the detectable molecule.

161. The method of claim 160, wherein the analyzer is a FACS analyzer.

162. The method of claim 160, wherein the analyzer is a capillary-based screening apparatus.

163. The method of claim 160, wherein the analyzer is a mass spectroscopic screening apparatus.

164. A method for identifying a bioactivity or biomolecule of interest, comprising:

a) running the extract of a library containing a plurality of clones comprising polynucleotides derived from a mixed population of organisms or more than one organism, through a column;

b) transferring the extract to a first host cell;

c) contacting the extract with a second host cell containing a detectable reporter molecule; and

d) measuring the mass spectra of the host cell with the extract, wherein a difference in the mass spectra of the host cell with the extract from the mass spectra without the extract is indicative of the presence of a bioactivity or biomolecule of interest in the extract of the library.

165. A sample screening apparatus, comprising:

a plurality of capillaries held together in an array, wherein each capillary comprises at least one wall defining a lumen for retaining a sample;

interstitial material disposed between adjacent capillaries in the array; and

one or more reference indicia formed within of the interstitial material.

166. The apparatus of claim 165, wherein each capillary has an aspect ratio of between 10:1 and 1000:1.

167. The apparatus of claim 166, wherein each capillary has an aspect ratio of between 20:1 and 100:1.

168. The apparatus of claim 165, wherein each capillary has an aspect ratio of between 40:1 and 50:1.

169. The apparatus of claim 165, wherein each capillary has a length of between 5mm and 10 cm.

170. The apparatus of claim 165, wherein the lumen of each capillary has an internal diameter of between 3μm and 500μm.

171. The apparatus of claim 165, wherein the lumen of each capillary has an internal diameter of between 10μm and 500μm.

172. The apparatus of claim 165, wherein the plurality of capillaries are fused together to form the array.

173. The apparatus of claim 165, wherein the reference indicia are formed at intervals of a number of capillaries.

174. The apparatus of claim 165, wherein the reference indicia are formed at edges of the array.

175. The apparatus of claim 165, wherein the reference indicia are formed of glass.

176. A capillary for screening a sample, wherein the capillary is adapted for being held in an array of capillaries, the capillary comprising:

a first wall defining a lumen for retaining the sample, wherein the first wall forms a waveguide for propagating detectable signals therein; and

a second wall formed of a filtering material, for filtering excitation energy provided to the lumen to excite the sample.

177. The capillary of claim 176, wherein the second wall circumscribes the first wall.

178. The capillary of claim 176, wherein the second wall is formed of extra mural absorption (EMA) glass.

179. The capillary of claim 178, wherein the EMA glass is tuned to filter specific wavelengths of light.

180. A capillary array for screening a plurality of samples, comprising:

a plurality of capillaries, held together into the array, wherein each capillary includes a first wall defining a lumen for retaining the sample, and a second wall circumscribing the first wall, for filtering excitation energy provided to the lumen to excite the sample.

181. The array of claim 180, wherein the second wall of each capillary is formed of a filtering material.

182. The array of claim 181, wherein the filtering material is EMA glass.

183. The array of claim 182, wherein the EMA glass is tuned to filter specific wavelengths of light.

184. The array of claim 180, further comprising interstitial material between adjacent capillaries.

185. The array of claim 184, wherein the interstitial material is adapted to absorb light.

186. A method for incubating a bioactivity or biomolecule of interest, comprising:

introducing a first component into at least a portion of a capillary of a capillary array, wherein each capillary of the capillary array comprises at least one wall defining a lumen for retaining the first component;

introducing air into the capillary behind the first component; and

introducing a second component into the capillary, wherein the second component is separated from the first component by the air.

187. The method of claim 186, wherein either the first or second component includes at least one particle of interest.

188. The method of claim 187, wherein the other of the first and second component includes a developer for causing an activity of interest by the particle of interest.

189. The method of claim 187, wherein the particle of interest is a molecule.

190. The method of claim 186, further comprising disrupting the air to combine the first component with the second component.

191. The method of claim 186, wherein the first and second components are liquids.

192. A method of incubating a sample of interest, comprising:

introducing a first liquid labeled with a detectable particle into a capillary of a capillary array, wherein each capillary of the capillary array comprises at least one wall defining a lumen for retaining the liquid and the detectable particle;

submersing one end of the capillary into a fluid bath containing a second liquid; and

evaporating the first liquid from the opposite end of the capillary to draw the second liquid into the capillary tube.

193. The method of claim 192, wherein the second liquid contains a developer for causing an activity of interest by the detectable particle.

194. The method of claim 193, wherein the developer includes at least one nutrient.

195. The method of claim 194, wherein the nutrient includes oxygen.

196. A method of incubating a sample of interest, comprising:

introducing a first liquid labeled with a detectable particle into a capillary of a capillary array, wherein each capillary of the capillary array comprises at least one wall defining a lumen for retaining the first liquid and the detectable particle, and wherein the at least one wall is coated with a binding material for binding the detectable particle to the at least one wall;

removing the first liquid from the capillary tube, wherein the bound detectable particle is maintained within the capillary; and

introducing a second liquid into the capillary tube.

197. The method of claim 196, wherein the binding material includes DNA.

198. The method of claim 197, wherein the binding material includes an antibody.

199. A method of incubating a sample of interest, comprising:

introducing a liquid labeled with a detectable particle into a capillary of a capillary array, wherein each capillary of the capillary array comprises at least one wall defining a lumen for retaining the liquid and the detectable particle;

introducing paramagnetic beads to the liquid; and

exposing the capillary containing the paramagnetic beads to a magnetic field to cause movement of the paramagnetic beads in the liquid within the capillary.

200. The method of claim 199, further comprising reversing polarity of the magnetic field to cause reverse movement of the paramagnetic beads.

201. A method of recovering a sample from one of a plurality of capillaries in a capillary array, comprising:

determining a coordinate position of a recovery tool;

detecting a coordinate location of a capillary containing the sample;

correlating, via relative movement between the recovery tool and the capillary containing the sample, the coordinate position of the recovery tool with the coordinate location of the capillary; and

providing contact between the capillary and the recovery tool.

202. The method of claim 201, further comprising removing, with the recovery tool, the sample from the capillary containing the sample.

203. A recovery apparatus for a sample screening system, wherein the system includes a plurality of capillaries formed into an array, the apparatus comprising:

a recovery tool adapted to contact at least one capillary of the capillary array and recover a sample therefrom;

an ejector, connected with the recovery tool, for ejecting the recovered sample from the recovery tool.

204. The recovery apparatus of claim 203, wherein the recovery tool includes a needle connected with a collection container.

205. The recovery apparatus of claim 203, wherein the recovery tool includes an aspirator for recovering the sample.

206. The recovery apparatus of claim 203, wherein the ejector includes a jet mechanism adapted to expel the recovered sample.

207. The recovery apparatus of claim 203, wherein the jet mechanism is operable by thermal energy applied thereto.

208. The recovery apparatus of claim 207, further comprising a heating element connected to the jet mechanism.

209. A sample screening apparatus, comprising:
a plurality of capillaries held together in a planar array, wherein each capillary comprises at least one wall defining a lumen for retaining a sample;

interstitial material disposed between adjacent capillaries in the array; and
one or more reference indicia formed within of the interstitial material.

210. The sample screening apparatus of claim 209, wherein the planar array includes approximately 1,000,000 capillaries.

211. A method of enriching for a polynucleotide encoding an activity of interest, comprising: contacting a mixed population of polynucleotides derived from a mixed population of organisms with at least one nucleic acid probe comprising a detectable label and at least a portion of a polynucleotide sequence encoding a polypeptide of interest having a specified activity to enrich for polynucleotides positive for a sequence of interest.